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Genetic profiling of chromosome 1 in breast cancer : mapping of regions of gains and losses and identification of candidate genes on 1q

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Abbreviations : BAC; bacterial artificial chromosome. CGH ; comparative genomic hybridization. CNC ; copy number change. CNI; Copy Number Increase. SRO; Shortest Region of Overlap. cDNA ; complementary DNA. FISH ; fluorescent in situ hybridization. ER ; estrogen receptor. DS; Discriminating Score.

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Abstract

Chromosome 1 is involved in quantitative anomalies in 50-60% of breast tumors. However, the structure of these anomalies and the identity of the affected genes remain to be determined. To characterize these anomalies and define their consequences on gene expression, we undertook a study combining array-CGH analysis and expression profiling using specialized arrays. Array-CGH data showed that 1p was predominantly involved in losses and 1q almost exclusively in gains. Noticeably, high magnitude amplification were infrequent. In an attempt to fine map regions of copy number changes we defined 19 shortest regions of overlap (SRO) for gains (1 at 1p and 18 at 1q) and of 20 SROs for losses (all at 1p). These SROs, whose sizes ranged 170 Kb to 3.2 Mb, represented the smallest genomic intervals possible based on the resolution of our array.

The elevated incidence of gains at 1q, added to the well established concordance between DNA copy increase and augmented RNA expression made us focus on gene expression changes at this chromosomal arm. To identify candidate oncogenes, we studied the RNA expression profiles of 307 genes located at 1q using a home-made built cDNA array. We identified 30 candidate genes showing significant overexpression correlated to copy number increase. In order to substantiate their involvement, RNA expression levels of these candidate genes were measured by quantitative RT-PCR in a panel of 25 breast cancer cell lines previously typed by array-CGH. Q-PCR showed that 11/29 genes were significantly overexpressed in presence of a genomic gain in these cell lines, while 21/28 genes were overexpressed when compared to normal breast.

Introduction

Chromosome 1 is recurrently altered in a number of human malignancies. In solid tumors structural aberrations include several recurrent chromosomal translocation sites, as well as frequent gains or losses involving either chromosomal arm (Struski et al., 2002; Teixeira et al., 2002). In breast cancer, chromosome 1 is the site of rare stereotypic rearrangements; isochromosome i(1)(q10), and der(1; 16)(q10; p10) (Tsarouha et al., 1999). More significantly, it has been shown, by either LOH or CGH work, to be frequently involved in copy number changes (CNC) (Kerangueven et al., 1997; Osborne & Hamshire, 2000). Fifty to 60% of breast tumors analyzed by CGH presented gains at 1q, while the short arm showed predominantly losses, except the 1p31-p32 region which presented occasional gains (Courjal & Theillet, 1997; Tirkkonen et al., 1998). Gains at 1q frequently affect the whole arm, however, a number of tumors or cell lines exhibit interstitial gains sometimes reduced to a chromosomal band or subband (Courjal & Theillet, 1997; Larramendy et al., 2000). These data suggesting the existence at 1q of several regions of gains were thus concordant with LOH studies indicating the occurrence of at least 4 regions of allelic imbalance in breast tumors (Kerangueven et al., 1997). Because gains at 1q were observed both in low and high grade breast tumors, its implication in early stages of disease development has been shown (Cummings et al., 2000; Tirkkonen et al., 1998). Recent data using BAC based array-CGH on independent sets of breast tumors have confirmed the frequent nature of gains on chromosome 1, as well as the existence of multiple cores of amplification (Stange et al., 2006). Altogether these data suggested the presence of several important cancer genes on chromosome 1. Several known oncogenes (*NRAS*, *JUN*, *MYCL*, *TAL1*, *BLYM*, *LCK*) map on chromosome 1q, but their implication in breast cancer has remained elusive, while genes like *MUC1* and *PLU-1/JARIB1* were proposed as candidates (Bieche et al., 1997; Lu et al., 1999). However, it seems clear that most genes involved remain to be identified. This notion was reinforced by recent expression profiling studies in breast tumors that showed that 25

genes located on the long arm of chromosome 1 showed increased expression levels in conjunction to DNA copy number increase (CNI) (Hyman et al., 2002).

Our goal in this work was to determine more precisely the boundaries of regions of chromosome 1 showing copy number changes (CNC) in breast tumors and gain insight on genes involved. To achieve this, we built a genomic array covering both arms of chromosome 1 at an average density of 1 BAC clone/0.85 Mb and analyzed 30 breast cancer cell lines and 30 primary breast tumors by array-CGH. Based on the array-CGH profile we defined shortest regions of overlap of copy number gain or loss. A total of 20 regions of loss, all located at chromosome 1p, and 19 regions of gain, 1 at 1p and 18 at 1q, were defined. Because gains at 1q were found in over 60% of the analyzed samples and increased copy number are clearly related to augmented gene expression, we focused our expression study on the identification of candidate genes at 1q. To this aim we studied expression profiles of 307 known genes located on the long arm of chromosome 1. Using a supervised analysis method we selected 30 genes showing significantly increased RNA expression in relation to genomic gains. RNA expression levels of 28/30 genes were verified by Q-RT-PCR and the overexpression in relation to gains was confirmed for 11/28 genes, while 20/28 showed overexpression compared to normal breast.

Material and methods

Tumors and blood samples

30 breast tumors were obtained from the Pathology Department at the Val d'Aurelle Cancer Center of Montpellier (France). Tumor biopsies were snap-frozen in liquid nitrogen upon surgical removal and stored at -80°C until DNA and RNA extraction. Tumor cohorte was composed of 63.7% invasive ductal carcinoma, 18% invasive lobular carcinoma, 15% invasive adenocarcinoma of unspecified type and 3.3% others types carcinomas of the breast. The mean age of patients was 58 years. Tumors were mostly grade 2 and 3 (46,7% and 29,2% respectively), whereas 13,9% were grade 1 and 10% were uninformed.

Cell lines and tumors

Breast cancer cell lines used in this study included BRCAMZ01, MDAMB175, MDAMB453 (D. Birnbaum, Inserm U119, Marseille, France), CAL51, MDAMB435, SKBR7, ZR7530 (P. Edwards, Department of Pathology, Cambridge, UK), BT474, MCF7Rich (F. Vignon, Inserm U540, Montpellier, France), HS578T, MDAMB436, (A. Puisieux, Inserm U590, Lyon, France), SUM149, SUM185, SUM52 (S. Ethier, University of Michigan, Ann Arbor, MI, USA), EFM19, (DSMZ, Braunschweig - Germany), BT20, BT483, HCC1187, HCC1395, HCC1428, HCC1937, HCC1954, HCC2218, MDAMB157, MDAMB361, MDAMB468, SKBR3, T47D, UACC812, ZR751 (ATCC, American Type Culture Collection, Manassas, VA, USA). All cell lines were cultured as recommended by suppliers.

Genomic arrays

We built a genomic array covering chromosomes 1, 8 and 17. Coverage of chromosomes 8 and 17 has been described in (Gelsi-Boyer et al., 2005; Orsetti et al., 2004). Chromosome 1 was covered by 257 BAC clones selected as follows; 225 BAC clones from the Barbara Trask collection (CHORI) <http://www.ncbi.nlm.nih.gov/genome/cyto/hbrc.shtml> and 32 clones selected according to their cytogenetic position and content in genetic markers. Clones were arranged according to the human genome freeze of april 2003 (complete list available on request). This resulted in an average density of 1 clone/0.85Mb +/- 0.95Mb. However, clone

distribution was uneven and thus could produce local variations in resolution (a complete list of BAC clones with precise coordinates is available in Supplementary Table S1)

Arrays were produced according to the following procedure. BAC, PAC and Cosmid DNA was isolated using Nucleobond® BAC100 from Macherey-Nagel (Hoerd, France). Probe DNA to be spotted was prepared by DOP-PCR amplification on 10 ng of BAC matrix DNA in a final reaction volume of 100 µl. Primer sequences and DOP-PCR protocol used are available on the Sanger Center web site (<http://www.sanger.ac.uk/HGP/methods/cytogenetics/DOPPCR.shtml>) (Orsetti et al., 2004) .

We performed this with slight modifications : the second round DOP-PCR primer was not aminolinked. Purification of PCR products was done using Nucleofast® 96 PCR plates (Macherey-Nagel, Hoerd, France). Purified PCR products were resuspended in dd H₂O at 2µg/µl. An aliquot was run on an agarose gel in order to ascertain even distribution of the product in all the wells. Prior spotting products were diluted 1:1 in spotting solution (GE-Healthcare, Orsay, France) and spotted in quadruplicate onto Corning GapsII slides (Schiphol-Rijk, The Netherlands) using a Lucidea array spotter IV (Amersham Biosciences, Orsay, France).

Array-CGH probe labeling, hybridization, image capture and data analysis.

Genomic DNA was digested by NdeI according to the supplier's recommendations (Roche Diagnostics, Meylan, France). 300 ng of digested genomic DNA was labelled by random-priming in a 50µl reaction containing: 0.02mM dATP, 0.02mM dGTP, 0.02mM dTTP; 0.05mM dCTP; 0.04mM Cy3-dCTP or Cy5-dCTP; 25 Units of Klenow Fragment (50U/µl, New England Biolabs, Ozyme, Saint Quentin Yvelines, France), 10 mM -mercaptoethanol, 5mM MgCl₂, 50mM Tris-HCL pH 6.8 and 300µg/ml random octamers. The reaction was incubated at 37°C for 20 hours and stopped by adding 2.5µl EDTA 0.5M pH8. The reaction product size was about 100 bp. We purified labeled products using microcon 30 filters (Amicon, Millipore, Molsheim, France). Abundance of the labeled DNA was checked using a spectrophotometer and incorporation of dyes was calculated using Molecular Probes software (<http://www.probes.com/resources/calc/basedyerratio.html>). A mix of 700 pmol Cy5 and

700 pmol Cy3 labeled probes was ethanol precipitated in the presence of 250-300µg of human Cot-1 DNA (Roche Diagnostics, Meylan, France) and 100µg herring sperm DNA (Promega, Charbonnières, France). The pellet was dried and re-suspended in 110µl Hybrisol VII (Appligene Oncor, Qbiogen, Illkirch, France). The probes were denatured at 80°C for 10 min, and repetitive sequences were blocked by pre-annealing at 37°C for 30 min.

Slide processing was done using a HS4800 hybridization station (Tecan, Lyon, France). Slides were treated with a blocking buffer (5XSSC, 0.2%SDS, 1%BSA) at 42°C for 30 min and washed 3 times at 42°C using 2XSSC, 0.2%SDS. Preannealed probes were injected in the chambers and hybridization took place at 37°C for 16h with mild agitation. Posthybridization washes were as follows: 3 washes at 52.5°C in solution 1 (2XSSC, 0.2%SDS), followed by 3 washes in solution 2 (0.5XSSC, 0.2%SDS) and 1 wash in solution 3 (0.1XSSC) at 52.5°C. To remove salt and detergent residues a brief wash with dd water was performed at 37°C and slides were dried within the chambers by an injection of N₂ at 30°C.

Arrays were scanned by a GenIII Array Scanner (Amersham Biosciences, Orsay, France). Images were analyzed by ARRAY-VISION 6.0 software (Amersham Biosciences, Orsay, France). Spots were defined by use of the automatic grid feature of the software and manually adjusted when necessary. Fluorescence intensities of all spots were then calculated after subtraction of local background. These data were then analyzed using a custom made MS-Excel VBA script. Cy3 and Cy5 global intensities were normalized with the entire set of spots on the array, Cy3/Cy5 ratios were calculated, each BAC clone was spotted in 4 replicates, the median values of replicate spots were calculated and these values were used to define the selection threshold for individual spots. Only replicates showing less than 15% deviation from the median were kept and a clone was taken into consideration when at least 3 of 4 replicates showed values within the 15% deviation limit. Representation of profiles with log₂ ratios in Y-axis and Mb position of clones (<http://genome.ucsc.edu>, April 2003 freeze) along the chromosome in X-axis. For each sample, at least two experiments were performed (Cy3/Cy5 and Cy5/Cy3), and the final profile corresponds to the mean of two experiments.

RNA expression profiling of chromosome 1q using cDNA arrays

Variations in gene expression levels were analyzed by large-scale measurement with home-made cDNA mini-arrays (7.5 x 9 cm; 720 human genes; 11 genes/cm²) produced as described (Nugoli et al., 2003). More specifically our mini-arrays comprised 319 ESTs corresponding to 307 known genes mapping at 1q (Supplementary Table S2). Selection of cDNA clones was done according to Information gathered (and crosschecked) from different web based data bases Genemap: <http://www.ncbi.nlm.nih.gov/genemap99/>, Genecards: <http://genecards.weizmann.ac.il/>, Genelynx: <http://www.genelynx.org/> or UCSC Genome Browser, release april 2003: <http://genome.ucsc.edu/>. Hybridization signals were quantified using the HDG Analyzer software (Genomic Solutions, Ann Arbo, MI, USA) by integrating all spot pixel signal intensities and removing spot background values determined in the neighboring area.

Quantitative RT-PCR

RNAs from cell lines and normal breast samples used for real-time PCR were isolated using the RNeasy Minikit (Qiagen, France) in accordance with the supplier's conditions. One g of total RNA, treated beforehand with RNase-free DNase (Promega, France), was reverse transcribed using the SuperScript™ II RT and 250 ng of random hexamers (Invitrogen, France). Q-PCR reactions were carried out in an ABI Prism 7000 instrument (Applied Biosystems, France) in a final volume of 15 l according to the supplier's recommendations using SYBR Green as a detector. Primers were as described in Supplementary Table S3 in the supplementary data. We designed the primers for 17 genes, with the assistance of the Primer Express software (Applied Biosystems, France), and for the remaining 14 we used the Quantitect Primer Assays from the Gene Globe database (Qiagen, France). *ESRRG* primers were as described by (Ariazi et al., 2002). Standard curves were determined for each gene analyzed by use of serial dilutions from the same pool of cDNAs. Relative quantities were calculated referring to these curves and relative expression levels of each target gene was normalized to 28 S RNA.

Identification of aberrantly expressed genes in regions of CNC

We applied a supervised analysis scheme to identify genes significantly correlated to copy number changes. Sample selection was based on array-CGH profiles. For each consensus region, samples presenting at least 25% of the BACs included in the region with log2 ratio exceeding 0.25 were considered as amplified. For each available gene at 1q, we computed a discriminating score by comparing expression levels between the subgroup of samples presenting amplification (subgroup 1) and the subgroup of samples without amplification (subgroup2). Discriminating score (Golub et al., 1999) was defined as $DS = (M1 - M2) / (S1 + S2)$, where M1 and S1 represent mean and the SD of expression levels of one gene in subgroup 1, M2 and S2 in subgroup 2. Confidence levels were calculated by performing 1,200 iterative random permutations per gene as described previously (Bertucci et al., 2004). Significance threshold for expression differences was $DS \geq 0.32$ corresponding to < 0.01 false positive. For Quantitative PCR results we applied a t test analysis.

Results

Patterns of gains and losses at chromosome 1 in breast cancer

We analyzed genomic profiles of 30 primary tumors and 30 cancer cell lines by array-CGH using a home built array covering chromosome 1 at an average density of 1 clone/0.85 Mb, with some local variations resulting in higher density locally at 1q. All cell lines studied, pre-selected on the basis of classical CGH profiles, presented gains and/or losses at either 1p or 1q. Array-CGH profiles were in good concordance with classical CGH data, confirming the prevalence of losses on the short arm combined with gains at 1q. However, in contrast to classical CGH data, gains encompassing the whole 1q were rare, with profiles typically showing multiple subregions of gains (Figure 1 and supplementary data Figure S1). Most prevalent gains were at 1q21-q22, 1q23-q24, 1q32 and 1q42-q44, while losses were noticeably rare on the long arm (Figures 1 and 2). On average tumors and cell lines presented 1 to 3 regions of gains per sample (Figure 1).

Our aim was to define the cores of the different regions of CNC on chromosome 1 and, thus, it was important to determine their boundaries. Correspondingly, we delineated the shortest regions of overlap (SRO) involved in either gains or losses on the whole chromosome 1. We overlaid all the array-CGH profiles and searched for shortest overlaps shared by at least 6 independent tumors or cell lines. We defined 19 SROs of gains (1 at 1p and 18 at 1q) and 20 SROs of losses (all at 1p) whose sizes ranged 170 Kb to 3.2 Mb (Figure 1). Precise locations and BAC content are described in supplementary data (Table S4). However, it must be pointed out that the actual sizes of these regions of overlap may change according to the resolution of the array used to define them.

Although, gains were generally of low to moderate level, high magnitude amplifications were observed. Similarly, we observed high magnitude losses (Figure 1). We were interested to see whether high magnitude amplifications occurred at recurrent sites and, accordingly, defined 7 peaks of amplification, which all, except that at 1p12, matched with SROs (Figure 1). This discrepancy can be explained by the different criteria used to define peaks of amplifica-

tion and SROs. Whereas SROs required to be shared by at least 6 samples to be retained, peaks of amplification needed to occur in at least 3 tumors or cell lines.

Identification of candidate genes involved in copy number changes at 1q

Because the relation between genomic gains and increased RNA expression is well established and linked to a selective advantage for cancer cells, we concentrated our efforts on the identification of the genes showing significantly increased expression levels as a consequence of gains at 1q. To this mean, we analyzed RNA expression profiles of 307 genes located on chromosome 1q in 29 cell lines and 26 tumors using self-made cDNA arrays. We performed a supervised analysis aiming at selecting genes differentially expressed in tumors or cell lines presenting a gain. We formed groups of tumors and cell lines according to their “gain” or “no gain” status in each region. However, based on the 19 SROs this resulted in a large number of subclasses whose samples were too small to reach statistical significance. To obviate this problem we defined larger regions of gains, designated consensus regions, which encompassed several SROs. To do this, we determined the occurrence curve for gains at each target clone at 1q. We reasoned that ruptures and low points in the curve represented the boundaries of the different regions (Figure 2). We retained only the events whose occurrence exceeded the mean (horizontal bar on Figure 2) and boundaries were defined by vertical lines tangential to the occurrence curve. Seven (7) consensus regions of gains (G1 through G7), ranging 3.6 to 11 Mb and encompassing two to three SROs on average were defined at 1q (Table 1 and Figure 2). Gains located between 170 and 180 Mb were not considered because their occurrence was below the threshold. Of the 307 genes studied, 178 were located within the consensus regions of gains defined at 1q. To identify genes whose expression levels were significantly modified in relation to CNC we calculated the Discriminating Score (DS) followed by 1200 random permutations (gain vs. no gain) and our significance threshold for expression differences was $DS \geq 0.32$ corresponding to < 0.01 false positive. This resulted in the selection of 30 genes distributed in consensus regions G1 through G7 (Table 2). Interestingly, we noted that a number of the selected genes were lo-

cated in close vicinity to each other suggesting the existence of local clusters, possibly related to the existence of core regions of gain.

Candidate gene verification by Quantitative RT-PCR

In order to confirm expression profiling results we measured the RNA expression levels of 28/30 genes by Quantitative RT-PCR (Q-RT-PCR) in 25 cell lines typed by array-CGH. The *c1orf2* and *HNRPU* genes could not be studied because of unsuccessful primer design. In addition to the 28 genes selected from the cDNA array data we studied the recently identified candidate oncogene *RAB25* (Cheng et al., 2004), which is located in consensus region G2, in close vicinity to two of our candidate genes, *MAPBPIP* and *CCT3* (Table 2). A t test analysis revealed that only 5/29 genes showed p values ≤ 0.05 , indicative of significant expression differences in relation to gains. We reasoned that this may be due to small sample size (we had to restrict our Q-PCR analysis to the 25 cell lines because tumor RNAs were no more available) and decided to consider genes with p values ≤ 0.1 . This allowed us to pick out a total of 11 genes (Table 2). It was, however, noticeable that the *RAB25* gene was not selected in this test, while it was, when we compared mean expression levels in cancer cell lines to that in a series of 5 normal breast tissues expression (t test p value=0.002). We, thus, applied this test to the whole set of genes which revealed that 21/29 were significantly overexpressed in cancer cell lines compared to normal breast.

Discussion

Chromosome 1 is a prevalent site of numerical anomalies combining losses on the short arm and gains on the long one in breast carcinomas (Courjal & Theillet, 1997; Teixeira et al., 2002). Gains at 1q are found in over 50% of breast tumors. While being frequent in high grade breast cancer, they have been related to ER positive cancers (Loo et al., 2004; Rennstam et al., 2003) and have been suggested to occur early in the natural history of the disease (Buerger et al., 1999; Malamou-Mitsi et al., 1999). These particularities fostered our interest in characterizing the genomic regions involved in copy number changes and identifying genes at 1q whose expression was modified in relation to gains.

Array-CGH data presented here confirm chromosomal CGH results showing the duality on chromosome 1, with the short arm being mainly involved in losses and the long arm almost exclusively in gains. Our data clearly indicated the existence of multiple subregions of losses at 1p and of gains at 1q. In an attempt to define these subregions with greater precision and possibly delimitate their cores, we determined the shortest regions of overlap for gains (19 SROs) and losses (20 SROs) on chromosome 1, whose sizes ranged 170Kb to over 3 Mb. SROs were defined according to the classical LOH scheme, in order to narrow down genetic intervals encompassing candidate genes. Our data thus suggest that numerical anomalies at chromosome 1, be it losses or gains, are complex and involve a large number of subregions and possibly combinations of anomalies.

Although losses at 1p were observed in a sizeable portion of the tumors and cell lines, gains were notably prevalent. This was in full agreement with previous chromosomal CGH results by us and other groups (Courjal & Theillet, 1997; Larramendy et al., 2000; Malamou-Mitsi et al., 1999; Tirkkonen et al., 1998). Interestingly, gains at 1q were of low to moderate level with a lower prevalence of amplifications compared to other chromosomes. Furthermore, no sharp transitions were observed at the boundaries of amplification peaks at 1q, in contrast to chromosomes 8p or 17q, where such recurrent breakpoint sites were common (Gelsi-Boyer et al., 2005; Orsetti et al., 2004).

The relation between aberrant gene dosage and gene expression is well accepted and is best shown in case of copy number increase. The common nature of genomic gains (which include DNA amplification) in breast tumors indicates that it is an effective mechanism of positive genetic selection in cancer cells (Upender et al., 2004). By cDNA-array expression profiling, we identified 30 genes whose RNA expression was significantly increased in relation to genomic gains. Overexpression in presence of genomic gain could be confirmed only for 11 genes by quantitative-RT-PCR. We suspect that these numbers may be related to the small size of our sample. We had to restrict our Q-PCR verification to 25 cell line RNAs, because tumor RNAs were no more available. We noted that 21 genes presented significant overexpression when compared to normal breast, suggesting the involvement of a larger number of genes within our original selection. It was interesting to see that, to the exception (*PLU-1/JARID1B*) (Lu et al., 1999), all the genes identified in our study were newly proposed as candidate cancer genes. Furthermore, *MUC1* (Schroeder et al., 2004), a long known cell surface marker overexpressed in a sizeable fraction of breast tumors, and *KIF14* (Corson et al., 2005), a recently proposed candidate at 1q31, presented Discriminating Scores below the threshold and were excluded from our selection. Genes selected in our study belong to rather diverse functional groups, of which three appeared prevalent. The first corresponded to a broad collection of positive regulators of cell proliferation. They include *PIP5K1A*, *MAPBPIP*, *RAB25A*, *PCTK3*, *RAB4* and *MPZL1*. The second was made of genes whose products were related to transcriptional regulation or chromatin remodeling such as *USF1*, *JARID1B*, *TBX19* or *CROC4*. The third included genes involved in cellular trafficking *VPS45A*, *ARF1*, *LYST*, *CCT3* or basic cellular metabolism *CA14*, *ALDH9A1*. Note that *RAB25* has also been related to the activation of protein trafficking between the membrane and the endoplasmic reticulum (Cheng et al., 2005). Similar functional groups have been observed in other selections of genes involved in genomic gains or amplifications, thus, indicating the importance of activated transcription, increased signaling and protein trafficking or catabolism in cancer. However, 8/24 overexpressed genes did not belong to any of the above mentioned functional groups. While two genes, *PDZK1* and *MLLT11*, were clearly

relevant to cancer as both have been proposed as a candidate oncogenes in diverse haematological malignancies (Busson-Le Coniat et al., 1999; Inoue et al., 2004; Tse et al., 2004), 6 were more difficult to relate to cancer. Three corresponded to genetic determinants of genetic syndromes (*MTMR*, *DISC1*, *MTX1*) and the three others bore functions with no obvious link to cancer (*NENF*, *ENSA*, *TARBP1*).

We were interested to verify the concordance between our analysis and the recently described “Transcriptome Correlation Map” (Reyal et al., 2005), which defined groups of collinear genes showing coordinated expression. Their dataset indicated 235 genes presenting a significant Transcriptome Correlation Score (TCS) at 1q, of which 147 mapped within the region of gains defined in our work, of which 72 (48%) were located in G1 and G2 (1q21 or 1q22). Genes within consensus regions of gains presented a significantly higher TCS, thus being in accordance with the existence of a link between increased expression and copy number gains at 1q. This was further corroborated by the fact, that 14/30 (43%) genes selected by Discriminating Score showed significant TCS, which is an increase compared to the 55/178 (31%) genes common to both studies and located in the regions of gains. This suggested an enrichment of genes belonging the transcriptome correlation map in our set of candidate genes at 1q and contrasted to our previous findings at 8p (Gelsi-Boyer et al., 2005).

Despite their frequent nature, numerical anomalies affecting chromosome 1 in breast and other cancers have drawn less attention than deserved. Most studies focussed on specific subregions or candidate genes. In this work we characterized at high resolution regions recurrently involved in copy number alterations on chromosome 1 in breast cancer and identified 24 candidate genes overexpressed in regions of gains at 1q. To our knowledge, this is the first study mapping at high resolution regions of loss and gain on the whole length of chromosome 1 and proposing a series of candidate genes affected by copy number changes. Further work will need to ascertain the true relevance to breast cancer of these candidate genes. This will require bioclinical and functional studies. Moreover, since our

screen was based on a set of 307 known genes representing 40-50% of the genes assigned at 1q, our selection leaves way to the identification of additional candidate genes.

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Legends to Tables and Figures

Table 1: Description of consensus regions of gain at 1q. Consensus regions of gain were defined by the BAC bordering them, Mb start corresponds to the 5' end of the proximal BAC, Mb end to the 3' end of the distal BAC.

Table 2: Gene expression analysis at 1q and correlation with copy number gain. RNA expression profiles of 307 genes located at 1q were analyzed in a total of 29 breast cancer cell lines and 26 primary tumors. Genes presented correspond to the 31 genes selected by Discriminating Score. Significance threshold was $DS > 0.32$ corresponding to <0.01 false positive. Expression levels were quantified by Q-RT-PCR for 28/30 genes (primer design was unsuccessful for *c1orf2* and *HNRPU*). Q-PCR primers sequences are presented in supplementary Table S2. The recently reported candidate oncogene *RAB25*, which was not present on our array, was quantified as a positive control. Q-RT-PCR data were analyzed for differential expression using two t tests approaches; t test 1 (noted p value 1) indicates correlation with copy number gain; t test 2 (p value 2) differential expression with normal breast. Two significance thresholds were used; strict $p \leq 0.05$, tolerant $p \leq 0.1$, p values > 0.1 were considered as non significant and only values within the tolerance limit are indicated. Cell lines analyzed were; BRCAMZ01, MDAMB175, CAL51, MDAMB435, SKBR7, ZR7530, BT474, MCF7Rich, HS578T, MDAMB436, SUM149, SUM185, BT20, HCC1187, HCC1428, HCC1937, HCC1954, HCC2218, MDAMB157, MDAMB361, MDAMB468, SKBR3, T47D, UACC812, ZR751. ND = not done and refers to Q-RT-PCR measurements which could not be performed.

Figure 1: Profiles of gains and losses on chromosome 1 in breast cancer. Definition of shortest regions of overlap (SRO) and events of high magnitude. Grey horizontal lines represent regions of gains (top) or losses (bottom) observed in each tumor or cell line (minimum 2 BACs involved with a \log_2 ratio ≥ 0.25 or ≤ -0.25). SROs are indicated as bold grey bars

with gains above the chromosome ideogram and losses below. SROs correspond to the smallest overlap shared by at least six tumors or cell lines. Arrow heads indicate events of high magnitude, either peaks of amplification or loss. They corresponded to events with \log_2 ratio > 0.7 in at least 3 tumors or cell lines. Code for cell lines 1: BRCAMZ01, 2: BT20, 3: BT474, 4: BT483, 5: CAL51, 6: EFM19, 7: HCC1187, 8: HCC1395, 9: HCC1428, 10: HCC1937, 11: HCC1954, 12: HCC2218, 13: Hs578T, 14: MCF7Rich, 15: MDAMB157, 16: MDAMB175, 17: MDAMB361, 18: MDAMB435, 19: MDAMB436, 20: MDAMB453, 21: MDAMB468, 22: SKBR3, 23: SKBR7, 24: SUM52, 25: SUM149, 26: SUM185, 27: T47D, 28: UACC812, 29: ZR751, 30: ZR7530. Code for primary tumors 1: VA1593, 2: VA4055, 3: VA4380, 4: VA4390, 5: VA4435, 6: VA4956, 7: VA5033, 8: VA5077, 9: VA5101, 10: VA5410, 11: VA5450, 12: VA6088, 13: VA6190, 14: VA6204, 15: VA6219, 16: VA6277, 17: VA6582, 18: VA6586, 19: VA6660, 20: VA7079, 21: VA7106, 22: VA7417, 23: VA6052, 24: VA6094, 25: VA6138, 26: VA6143, 27: VA6270, 28: VA6403, 29: VA6603, 30: VA7072.

Figure 2 : Definition of consensus regions of gain at 1q. Consensus regions were based on the curve of cumulated occurrence of gains (\log_2 .ratio ≥ 0.25) at 1q in 30 cell lines and 30 primary tumors. Low points defined boundaries and high points possible cores. Only regions showing an occurrence exceeding the mean (9.0) were considered. Plots are based on the Mb positioning of the clones on the array. Hence clones positioned close to each other may appear as merged. Consensus regions of gains were designated G1 through G7 and represented as bold grey lines. Short grey lines represent the position of SROs relative to that consensus regions.

Table 1

Consensus Segments	Genomic Positions	Size (bp)	Cytoband	BAC names	SRO included	Number of genes on our array
G1					2-3	
start	143154718	5191576	1q21.1	CTD-2122l24		31
end	148346294		1q21.3	RP11-74C1		
G2					4	
start	150842537	3669729	1q21.3	RP11-73C10		36
end	154512266		1q23.1	RP11-91g5		
G3					5-6-7-8	
start	157448999	9571469	1q23.3	RP11-79m15		42
end	167020468		1q24.2	RP11-184n12		
G4					11-12-13	
start	194594372	7404055	1q31.3	RP11-321M13		33
end	201998427		1q32.1	CTD-2218h7		
G5						
start	208699401	5211392	1q32.3	RP11-216f1	14-15	8
end	213910793		1q41	RP11-260a10		
G6						
start	223358648	11257879	1q42.12	CTD-2148o23	16-17	19
end	234616527		1q43	RP11-80p14		
G7						
start	235845765	8332672	1q43	RP11-130i13	18-19	9
end	244178437		1q44	RP11-172p12		

Table 2:

Consensus segment	clone ID on the chip	Hugo gene symbol	Gene Name	Localisation (start-end) (bp)	Cytoband	p value 1	p value 2
G1	pdzk1	<i>PDZK1</i>	PDZ domain containing 1	143403500-143439848	1q21.1		0.015
G1	h2bfq	<i>HIST2H2B</i>	histone 2, H2be	146631105-146633327	1q21.2		
G1	cra	<i>MTMR11</i>	myotubularin related protein 11	146675639-146683822	1q21.2	0.09	0.011
G1	vps45b	<i>VPS45A</i>	vacuolar protein sorting 45A	146814958-146892599	1q21.2	0.025	0.027
G1	ca14	<i>CA14</i>	carbonic anhydrase XIV	147005313-147012571	1q21.2		0.019
G1	ensa	<i>ENSA</i>	endosulfine alpha	147370158-147377163	1q21.3	0.05	0.025
G1	anxa9	<i>ANXA9</i>	annexin A9	147729649-147743202	1q21.3		
G1	af1q	<i>MLLT11</i>	myeloid/lymphoid or mixed-lineage leukemia ; translocated to, 11	147807778-147816066	1q21.3		0.045
G1	pip5k1a	<i>PIP5K1A</i>	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	147897780-147948713	1q21.3	0.09	
G2	mtx1	<i>MTX1</i>	metaxin 1	151952587-151957144	1q22		0.051
G2	c1orf2	<i>C1orf2</i>	chromosome 1 open reading frame 2	151994882-152003120	1q22	ND	ND
G2	hspc003	<i>MAPBPIP</i>	mitogen-activated protein-binding protein-interacting protein	152802478-152806168	1q22	0.076	
G2		<i>RAB25</i>	RAB25, member RAS oncogene family	152808855-152818122	1q22		0.001
G2	cct3	<i>CCT3</i>	chaperonin containing TCP1, subunit 3 (gamma)	153056634-153085846	1q22		0.0003
G2	croc4	<i>C1orf61</i>	chromosome 1 open reading frame 61	153128056-153153185	1q22		0.075
G3	usf1	<i>USF1</i>	upstream transcription factor 1	157781513-157787199	1q23.3	0.009	0.007
G3	aldh9	<i>ALDH9A1</i>	aldehyde dehydrogenase 9 family, member A1	162327485-162364132	1q24.1	0.088	0.022
G3	mpz11	<i>MPZL1</i>	myelin protein zero-like 1	164387268-164453994	1q24.2	0.05	0.070
G3	tbx19	<i>TBX19</i>	T-box 19	164946309-164979694	1q24.2		0.027
G4	plu-1	<i>JARID1B</i>	Jumonji, AT rich interactive domain 1B (RBP2-like)	199162987-199245053	1q32.1	0.097	0.095
G4	sox13	<i>SOX13</i>	SRY (sex determining region Y)-box 13	200442674-200457500	1q32.1		
G4	pctk3	<i>PCTK3</i>	PCTAIRE protein kinase 3	201857380-201862760	1q32.1	0.05	0.001
G5	spuf	<i>NENF</i>	neuron derived neurotrophic factor	209222493-209235935	1q32.3		0.023
G5	esrrg	<i>ESRRG</i>	estrogen-related receptor gamma	212723109-213309462	1q41		
G6	arf1	<i>ARF1</i>	ADP-ribosylation factor 1	224655969-224672451	1q42.13	0.098	
G6	rab4	<i>RAB4A</i>	RAB4A, member RAS oncogene family	225806272-225839911	1q42.13		0.020
G6	disc1	<i>DISC1</i>	disrupted in schizophrenia 1	228235748-228635487	1q42.2		0.001
G6	tarbp1	<i>TARBP1</i>	TAR (HIV) RNA binding protein 1	230818923-230906713	1q42.2		0.0009
G6	tbce	<i>TBCE</i>	tubulin-specific chaperone e	231749924-231831433	1q42.3		
G6	chs1	<i>LYST</i>	lysosomal trafficking regulator	232120934-232326807	1q42.3		0.010
G7	hnrpu	<i>HNRPU</i>	heterogeneous nuclear ribonucleoprotein U	241218474-241229338	1q44	ND	ND

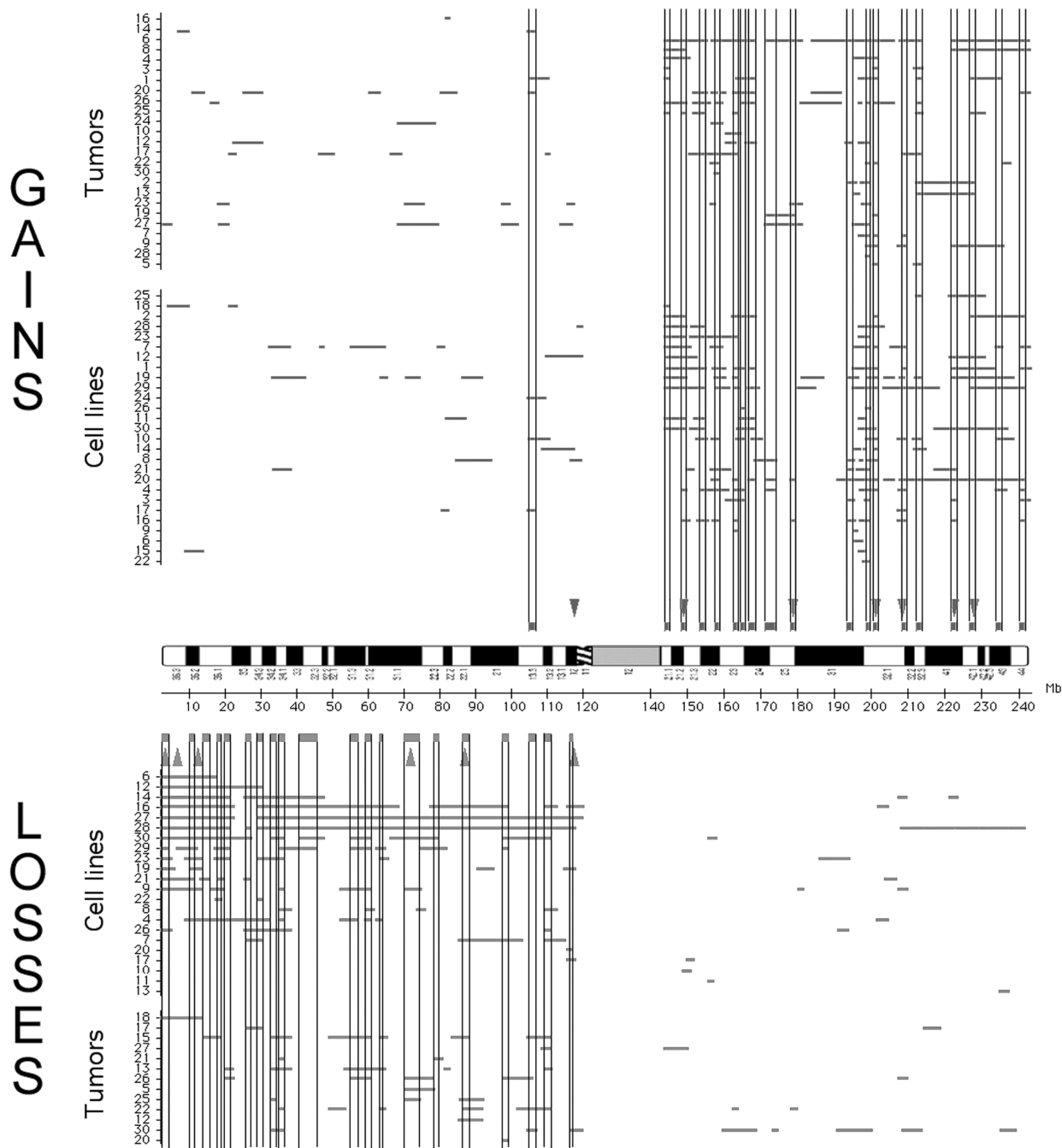


Figure 1

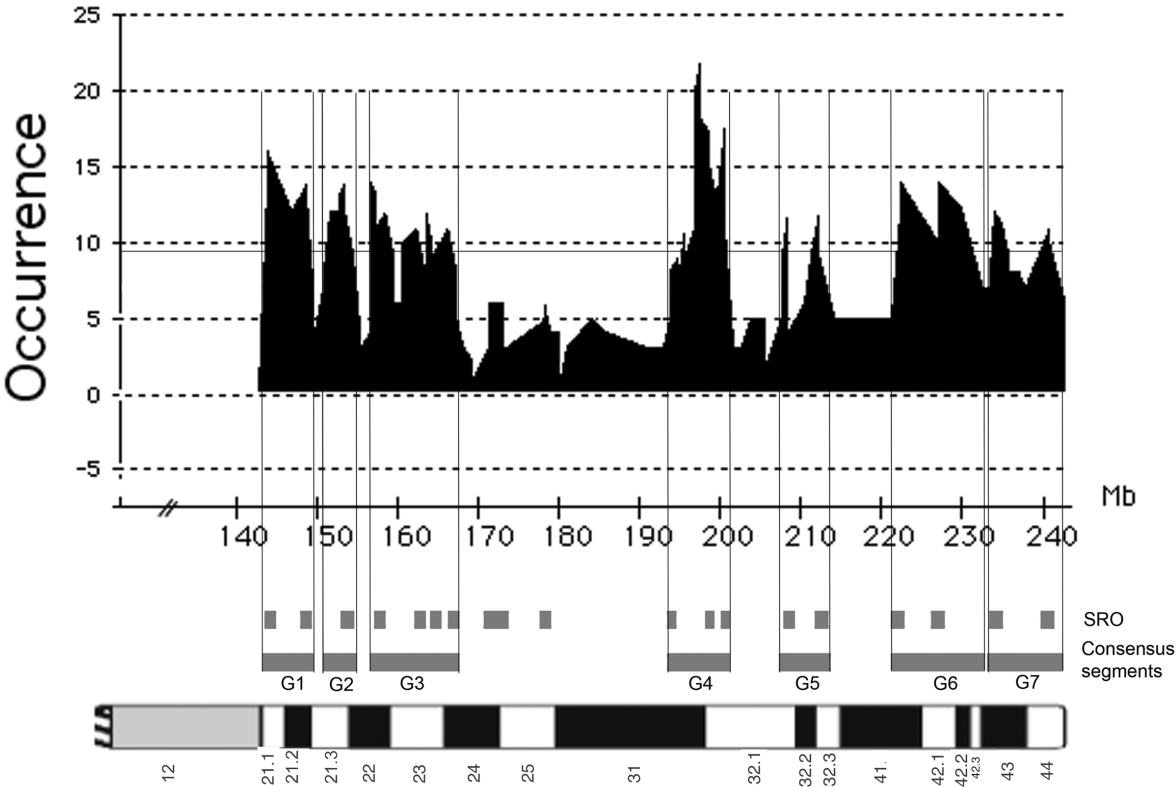


Figure 2